LOCALIZATION OF ALU SEQUENCES THAT MATCH TO THE GENOMIC REGIONS THAT EXHIBITED EVIDENCE FOR LINKAGE TO MAJOR PSYCHOSIS

SZ - Alu clones from individuals affected with schizophenia
BD - Alu clones from individuals affected with bipolar disorder
MD - major depression
CTRL - control samples

Sample Name (matched bp, %, chr	Homology length in bp; %	Chromosomal location	Evidence for linkage or association to schizophrenia or bipolar disorder
sites			
SZe-32m56	189, 99.5 %	. 6p22.3	Eckstein GN, Schwab SG, Maier W, Wildenauer DB. 1998. Searching
			for candidate genes for schizophrenia in chromosome 6p22,23: isolation of a BAC contig spanning 3.5 megabases. Am J Med Genet 81:530.
Sch37-9RR	160, 98.2 %	10p14	10p11-15 Faraone et al. (1998) nonparametric LOD scores at markers
			D10S1423 and D10S582 were 3.4 ($P = .0004$) and 3.2 ($P = .0006$),
			respectively.
E-283m56SZ	190, 99.5%	10p14	
	٠		Schwab et al. (1998a), 'nonparametric LOD score of 3.2 ($P = .0007$) at
			marker D1051/14(Scnwab et al. 1998)
			(Straub et al. 1998)Straub et al. (1998) LOD score of 1.91 ($P = .006$) at
			with markers D10S1426 and D10S674

Ledwab SG, Hallmayer J, Albus M, Lerer B, Hanses C, Kanyas K, Segman R, Borrman M, Dreikorn B, Lichterman D, Rietschel M, Tarker M, Maier W, Wildenauer DB. 1998. Further evidence for a susceptibility locus on chromosome 10p14-p11 in 72 families with Kanyiorgou M, Kasch L, Lasaster VK, Hwang J, Elango R, Bernardini DJ, Kimberland M, Babb R, Francomano CA, Wolynice PS, et al., (1994). Report from the Maryland Epidemiology Schizophrenia Linkage Study: no evidence for linkage between schizophrenia and a number of candidate and other genomic regions using a complex dominant model. Am J Med Genet 54:345-53 @ bunparametric linkage analysis. Am J Med Genet 81:302-307.

Figure

SZr-37m56	183, 96.5 %	11q14.2	Mulcrone J, Whatley SA, Marchbanks R, Wildenauer D, Altmark D, Daoud H, Gur E, Ebstein RP, Lerer B. 1995. genetic linkage analysis of
			schizophrenia using chromosome 11q13–24 markers in Israeli pedigrees. Am J Med Genet 60:103–108.
E-318_m74_SZ	206, 97.7%	22q12.2	22q11-13, Pulver et al. (1994a)(Pulver et al. 1994a; Pulver et al. 1994b; Pulver et al. 1994c) LOD score of 2.82 at marker locus IL2RB; (P = .009)
			The implicated region is near the velocardiofacial syndrome (VCFS) deletion,
			Lasseter et al. 1995(Lasseter et al. 1995)
			Polymeropoulos (Polymeropoulos et al. 1994)et al. 1994 Coon (Coon et al. 1994a; Coon et al. 1994b)et al. 1994a
			Stober (Stober et al. 2000)et al. 2000 Wides Worslaw et al. 1000) et al. 1000
E-305 m740 SZ	191, 100 %	Ya12, Ya11.23.	Yol 1.23 and Yol 2 (Alitalo et al. 1988) Alitalo T. Tiihonen J. Hakola P.
E-221_m37_SZ		Yq11.223	de la Chapelle A. 1988
E-267 m50 Ctrl			•
E-288 m56 SZ			
E-289_m56_SZ			
E-297_m740_SZ			
E-295 m740 SZ			
E-294_m740_SZ			•
E-293_m56_SZ			
E-286_m56_SZ			
E-252_m48_SZ			
E-244 m48 SZ			
E-130_m37_SZ			· ·
SZm74-E-59			
SZm74-E-58			

Figure 1 Continued

SZm74-E-50			
SZbM37-1			
SZbM37-7			
SZCM37-5			
SZC- M37-2			
SZCM37-26		•	•
SZCM37-15			
SZC- M37-7			
SZC- M37-5			
SZD- M37-14			
SZRevCom48 E -33			
SZRevCom48 E-39			
SZm37-E-13 m37-7		,	
Sch37-1			
Sch37-6	·	•	-
Sch37-7			
E-284m56SZ			
E-267_m50_Ctrl	191, 100 %	Yq12, Yq11.23,	Yq11.23 and Yq12(Alitalo et al. 1988) Alitalo T, Tiihonen J, Hakola P,
E-261_m50_Ctrl		Yq11.223	de la Chapelle A. 1988
E-167m50Ctrl			
E-275m50Ctrl			
E-281m50Ctrl			
RevE-270m50Ctrl			
		(O)	CONTROLS
Ctrlm57-E-6	187; 99%	1431.1	D1S2141 1q32-q41 Hovatta et al. (1998) (Hovatta et al. 1998) 1q32-41
RevE-169m50Ctrl	179, 94.8%	1931.1	Hovatta et al. (1999) (Hovatta et al. 1999) LOD score of 3.82 at marker D1S2891

Figure 1 Continued

E-271m50Ctrl	155, 90.6 %	1432.1	
			Schizophrenia Hovatta et al. (1998) (Hovatta et al. 1998) D1S2141 1q32-q41 Lod score 90% penetrance Lod score = 3.73
Ctrlm50E-49	185, 98 %	2q35	Event-related brain potential P3 Almasy et al. (1998)(Almasy and Blangero 1998) Between D2S425 and D2S434 2q33-q37 Bivariate quantitative linkage analysis Lod score = 3.28
Ctrlm57-E-3.	191, 100 % or 189, 99.5 %	5q33.2 18q22.2	5q22-31 5q31 LOD score of 3.35 ($P = .0002$) at marker D5S804 5q23.3 Straub et al. (1997) (Straub et al. 1997)
			Marker D5S399 at 5q31
			5q31.3-q35.1 was presented by Shink et al. [1998] (Morissette et al. 1999)
			Shink E, Morissette J, Rochette D, Bordeleau L, Plante M, Villeneuve
			Barden N. 1998. Bipolar affective disorder susceptibility loci on chromosomes 5 and 21: heterogeneity in a homogeneous population in Quebec.

Figure 1 Continued

					<u>-</u>			
13q14-32, Blouin et al. (1998)(Blouin et al. 1998) nonparametric LOD score of 4.18 ($P = .00002$), near D13S174 on 13q32	Brzustowicz et al. (1999) ³ Ewald et al. [1998] found increased haplotype sharing with distal markers at 18q23 in eight BPI patients from the Faroe Islands, in a region also suggested by Freimer et al. [1996].	18p11.2 and 18q12.1-q12.3 for BP and SZ., *Gershon et al. [1998] WCPG High density screen chromosome 18; average density 3.25 cM BP: 22 multiplex BP families [see (Berrettini et al. 1994)Berrettini et al.	1994] c ASM I: DIT, DITS, CASMI: highest peak on 18p11.2 (lod Nonparametric analysis (ASPEX) c ASMI: highest peak on 18p11.2 (lod 4 2.32; p 4 0.00054) c ASMII: smaller peak closer to 18ptel (lod 1.44; p 4 0.005) c Smaller peak at 18q21 (lod □□1; not significant) c 4 0.005) c Smaller peak at 18q21 (lod □□1; not significant) c Confirmation previous evidence for linkage to 18p11.2 Confirmation previous evidence for linkage to 18p11.2	22q11-13, Pulver et al. (1994a)(runvel et al. 1994) Pulver et al. 1994c) Pulver et al. 1994c) 1. OD score of 2.82 at marker locus IL2RB	same general region ($P = .009$) The implicated region is near the velocardiofacial syndrome (VCFS) deletion, I asseter et al. 1995(Lasseter et al. 1995)	Polymeropoulos (Polymeropoulos et al. 1994)et al. 1994 Coon (Coon et al. 1994a; Coon et al. 1994b)et al. 1994a Stober (Stober et al. 2000)et al. 2000	Myles-Worsley(Myles-Worsley et al. 1999) et al. 1999	Figure 1 Continued
13q14.11	18q23	18p11.23		22q12.2				Fim
186, 97.4 %	181, 100 %	132, 94.7 %		193, 100 %				
Ctrlm57-E-5.	E-166m50Ctrl	E-279m50Ctrl		Ctrlm57-E-4				

Figure 1 Continued

22 11 12 Baron (Baron 1990) Baron 1995) 1990, 1993; Daton et al	(Baron et al. 1990), 1990; Risch (Risch 1990a; Risch 1990b)1990a; (Baron et al. 1993), 1993; Spence (Spence et al. 1993)et al. 1993; Cloninger (Cloninger 1994) 1994; Lander and Kruglyak 1995(Lander	and Kruglyak 1995); Owen and Craddock (Owen and Craddock 1996) 1996).	
12 Donon (Baron 10	(Baron et al. 1990). 1990; Pauls (Pauls 1993)1993; Cloninger (Cloninger 1993)	and Kruglyak 1995); Owen and Craddock (Ow	
	22q13.2		
	155, 87.5 %		
	Ctrlm57-6-E-1		

			23. 21. 22 Charactivility Locus for Bipolar and Unipolar Affective
BD43-15	190, 98.7 %	21 q 21.3	C21421-22 Susceptions, 2000. Disorders Repeated From Gurling [1998](Gurling 1998),
			1921-22 Brzustowicz et al. (2000)(Brzustowicz et al. 2000; Maziade et
BD43-6	190; 99%	1.1201	al. 2002) heterogeneity LOD score of 6.50 was found between markers al. 2002) heterogeneity LOD score of 6.50 was found between markers al. 2002) have et al. 1998)
			1q21 Dror et al. 1999(Dror et al. 1999) A potassium-channel gene
			(Hkca3/KCNN3) mapped to 1q21 - Austin et al. 1999). (- hKCa3/KCNN3) (Austin et al. 1999)
RevE-77m43BD	191, 99.5 %	1p31.1	Bipolar disorder Rice et al. (1991) Distorte tpor par etc from MLOD2.5
			. 2202 mi 1 1008) D28405 2022. 1
BDd_M34-14BD(187, 99 %	2p23.2).	Schizophrenia Blouin et al. (1998) (Blouin et al. 1909) Schizophrenia Blouin et al. (1998) (blouin et al. 1909) Nonparametric lod score NPI = 1.26 ($p = 0.104$)
E-79m43BD	186, 96.9 %	2q37.3	Event-related brain potential P3 Almasy et al. (1998)(Almasy and Blangero 1998) Between D2S425 and Almasy et al. (1997). Discrete grantitative linkage analysis Lod score
			3.28
dido, o	102 100 %	5a13.2:	5q11-13 Sherrington et al. (1988)(Sherrington et al. 1988a; Sherrington
E-78m43BD	172, 100 /0		1 0 0000

Figure 1 Continued

E-83m43BD	192, 100 % 192, 100 %	5q22.2; 5q13.3;	et al. 1988b), British and Icelandic pedigrees (a LOD score of 6.49, under a dominant model Maximum LOD score of 4.37 at locus D5S111
	192, 100 %	16q23.1	5q11-13 Silverman ⁷ et al. (1996)(Silverman et al. 1996) (Straub et al. 1997), (Bennett et al. 1997) Straub RE, MacLean CJ, O'Neill FA, Walsh D, Kendler KS. 1997.
			Support for a possible schizophrenia vulnerability locus in region 5q22-31 in Irish families. Mol Psychiatry 2:148–155.
			Bennett RL, Karayiorgou M, Sobin CA, Norwood TH, Kay MA. 1997. Am J Hum Genet 61:1450–1454.
BDd_M34-19BD.	192, 100 %	10p14 or 10p13	10p11-15 Faraone et al. (1998) nonparametric LOD scores at markers D10S1423 and D10S582 were 3.4 ($P = .0004$) and 3.2 ($P = .0006$), respectively.
			Schwab et al. (1998a), 8 nonparametric LOD score of 3.2 ($P = .0007$) at marker D10S1714(Schwab et al. 1998)
			(Straub et al. 1998) Straub et al. (1998) LOD score of 1.91 (P = .006) at with markers D10S1426 and D10S674
E-62m34BD	192, 100 %	10p14	10p11-15 Faraone et al. (1998) nonparametric LOD scores at markers D10S1423 and D10S582 were 3.4 (P = .0004) and 3.2 (P = .0006), respectively.
			Schwab et al. (1998a); 9 nonparametric LOD score of 3.2 ($P = .0007$) at marker D10S1714(Schwab et al. 1998)
			(Straub et al. 1998) Straub et al. (1998) LOD score of 1.91 ($P = .006$) at with markers D10S1426 and D10S674

Figure 1 Continued

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	191, 100 %	Yq12, Yq11.23, Yq11.223	Yq11.23 and Yq12(Alitalo et al. 1988) Alitalo T, Tiihonen J, Hakola P, de la Chapelle A. 1988
BD43-2 MDC- M39-2 MDD- M39-14 MD39-4 MD39-6 MD39-8 MD39-10	191, 100 %	Yq12, Yq11.23, Yq11.223	Yq11.23 and Yq12(Alitalo et al. 1988) Alitalo T, Tiihonen J, Hakola P, de la Chapelle A. 1988

GENES LOCATED IN THE CLOSE VICINITY TO THE CLONED ALU SEQUENCES

SZ - Alu clones from individuals affected with schizophenia BD - Alu clones from individuals affected with bipolar disorder

MD - major depression

CTRL - control samples

References in the brackets in the right hand side column indicate the papers in which implication of the detected genes in major psychosis

was discussed.

			Ganga language in the close vicinity
Clone Name	Homology length in	оша	Genes rocarcu in inc constant (within 100,000 bp)
	bp; %	I location	the state of the s
E-285_m56_SZ	198; 99.5%	1q31.1	Prostagianum-cardy process, 1997 #2; Geling, 1991 #3}
E-290 m56 SZ	189: 99.5%	1q31.1	DVB?
E-1/0 m48 SZ	197: 99.5%	1q42.3	ryanodine receptor 2 (cardiac), 10.1 10.
E 15/ m56 S7	188: 99%	2q33.1	general transcription factor III., pulypopulates,
SZcRev M37-6	187; 99%	5q14.1	MSH3, mutS (E. coli) nomolog 3 CENPH, kinetochore protein CENP-H
			CFDP1, craniofacial development protein 1 (Goodman, 1996 #4)
			IL1A, interleukin 1, alpha
			CRHBP, corticotropin releasing hormone-binding protein
	100 00 5 07	6n22.3	Ataxin 1, SCA1 6 papers found on Schizophrenia. 3 items 10mm on orporation
SZe-32m56	189, 39.3 70		{Culikovic, 2000 #100;Li, 1999 #101;Joo, 1999 #102;Fujana, 1997
			#103;Morris-Rosendahl, 1997 #104;Wang, 1996 #105} {Morris-Rosendam,
	•		1997 #40;Fernandez Piqueras, 1995 #41}
T 211 m7/ C7	201 100%	8p21.3	docking protein 2, 56kD, DOKZ
C70 25m56	189 99.5 %	8q24.23	hypothetical protein FLJ10901, FLJ10901
000 T	102 100%	7 ₀ 22.3	C4S-2, chondroitin 4-O-sulforransierase 2.
比-377 国-775-日	172, 10076	•	EIF3S9, eukaryotic translation initiation factor 3
07 11 10	196 00 5 %	8p23.1	hypothetical protein MGC16279
SZM/4-E-00.	100, 27.2 /2		

SZr-37m56	183, 96.5 %	11q14.2	embryonic ectoderm development, EED
E-310_m74_SZ	192, 100 %	14q21.3	ribosomal protein S29, RPS29 {Gentry, 2000 #49; Watanabe, 1996 #50} {Watanabe, 1994 #106}
E-313 m74 SZ	207, 97.7 %	15q26.3	MADS box transcription enhancer factor 2,, MEF2A {Turner, 1997 #109}
E-258 m48 SZ	199, 98.6 %	17q21.33	distal-less homeobox 4, DLX4
E-16 m37 SZ	191, 99.5%	17923.2	tousled-like kinase 2, TLK2
E-319_m74_SZ	% 001 °961	18p11.32	Hypothetical protein FLJ23017, FLJ23017
			highly expressed in cancer, rich in leucine, HEC
E-315_m74_SZ	191, 100 %	19q12	ubiquinol-cytochrome c reductase, Rieske, UQCRFS1 (Johnston-Wilson,
E-321 m74 SZ E-315 m74 SZ			2000 #53}
E-315_m74_SZ	191, 100 %	19p13.2	hypothetical protein FLJ14356, FLJ14356
E-321 m74 SZ			gonadotropin inducible transcription, GIOT-2
E-315 m74 SZ			Kruppel-type zinc finger (C2H2), ZK1
E-251_m48_SZ	198, 99.5 %	19p13.11	hypothetical protein FLJ13659, FLJ13659
<u>ь</u>	189, 100%	19p13.11	
2531_m48_SZ F_	188, 98.5%	19p13.11	
2532 m48 SZ	٠	,	
E-325 m74 SZ	204, 96.7 %	19p13.11	hypothetical protein FLJ13659
E-178_m74_SZ	205, 98.1 %	19q13.12	zinc finger protein HZF10, ZNF345 Takase, 2001 #54;Ogura, 2001 #55;Sun, 2001 #56
E-246 m48 SZ	192, 100 %	20p12.3	hypothetical protein MGC4816, MGC4816
SZd M37-3.	190, 100 %	20q13.2	LOC57167, similar to SALL1 (sal (Drosophila)-like
SZd M37-10.	190, 97.9 %	20q13.2	LOC57167, similar to SALL1 (sal (Drosophila)-like
E-318 m74 SZ	206, 97.7 %	22q12.2	oncostatin M, OSM
E	191, 100 %	Yq12,	variable charge, Y chromosome, 2 protein, VCY2
302 m/40 SZ		Yq11.23,	

Figure 2 Continued

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T 701 27 C7	V211 222					
E-241 III.) 34	C77.1.h1			•		
E-288 m56 SZ					,	
E-289_m56_SZ						
山		•				
297_m740_SZ						
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295_m740_SZ						•
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294 m740 SZ					·	
E-293 m56 SZ						
E-286 m56 SZ						
E-252 m48 SZ						
E-244 m48 SZ			·			
E-130 m37 SZ		-			•	
SZm74-E-59						
SZm74-E-58						
SZm74-E-50		•				
SZb- M37-1						
SZb-M37-7					٠	
SZC- M37-5						
SZC- M37-2						
SZCM37-26						
SZCM37-15						
SZC-M37-7	. '					 -
SZC- M37-5				•		
SZD-M37-14						
SZRevCom48						
E-33			•			•
SZRevCom48						
E-39						
SZm37-E-	٠					
13 m37-7						

Figure 2 Continued

Ctrlm57-E-2	163,91%	19a13.32	SULT2B1, sulfotransferase family, cytosolic, 2B, member
E-296 m57 Ctrl	179, 98.4 %	21q22.11	hormonally upregulated Neu-associated kinase, HUNK
Ctrlm57-E-4.	193, 100 %	22q12.2	OSM, oncostatin M (Ref?? 2 papers found on bipolar WHAT??).
			LIF, leukemia inhibitory factor (cholinergic
-			EPI64, EBP50-PDZ interactor of 64 kD
			SF3A1, splicing factor 3a, subunit 1, 120kD
Ctrlm57-6-E-1	155, 87.5 %	22q13.2	E1A binding protein p300, EP300
E-267_m50_Ctr1	191, 100 %	Yq12,	variable charge, Y chromosome, 2 protein, VCY2
E-261_m50_Ctrl		Yq11.23,	
E-167m50Ctrl		Yq11.223	•
E-275m50Ctrl			
E-281m50Ctrl			
RevE-			
270m50Ctrl			
BDd_M34-	187; 99%	2p23.2	BRE, brain and reproductive organ-expressed (TNFRSF1A.
14BD			LRRFIP1, leucine rich repeat (in FLII) interacting
4, 0, 0,0	707 00 001		
BD43-10	192: 99.1%	3p22.2	
			SEC22C, vesicle trafficking protein, isoform a
	181; 97.4%	3p22.1	-
E-74m43BD	195, 99.5 %	9q22.2	SHC3, neuronal Shc
BDc_M34-4BD	191, 100 %	11q11	FOLR1, folate receptor 1 precursor
	or 191, 100 %	11q13.4	SKD3, suppressor of potassium transport defect 3
BDc_M34-3BD			INPPL1, inositol polyphosphate phosphatase-like 1
			FOLR2, folate receptor 2 precursor.
			ARIX, aristaless (Drosophila) homeobox
BD43-8	178, 100 %	11q22.3	nuclear protein, ataxia-telangiectasia locus, NPAT {Lange, 1989 #114; Weeks,
	-		1989 #115}
E-72m43BD	160, 100 %	16q13	CNGB1, cyclic nucleotide gated channel beta 1
BD43-14	191, 100 %	16924.2	hypothetical protein FL J23497

Figure 2 Continued

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E-71m39MD	147, 92 %	15026 1	DRC1 mention and the first in the second sec
BDd M43-	201, 100 %	19n13 11	TACA, protein regulator of cytokinesis 1
19BD.		11.01471	Schizophrenia. 2 items found on bipolar.
·			Section, solute carrier family 5 (sodium iodide.
			L.12RB1, interleukin 12 receptor, beta 1 (41 papers found. on interleukin
BDC- M34-	191, 100 %	Yq12,	variable charge, Y chromosome, 2 protein, VCY2
BDC-M34-		rq11.23, Yq11.223	
BD34-5			
BD34-8			
BD43-1			•
BD43-2			
MD20.4			
MD39-4			
MD39-8			
MD39-10	_		
MDC- M39-2			
MDD-M39-14			
(190, 100)			
E-66m39MD			

Cloned Alu sequences

SZ- from individuals affected with schizophrenia CNTR- from control samples BD - from individuals affected with bipolar disorder MD - from individuals affected with major depression

ATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCACAGGTTCAAG CGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGT TGATTCCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTTGTATTTT AGTAGAGACCAGGATTCTTCATGTTGATAAGGTGGTTCTTGAACTCCTGACCTCAGATGATCCATCTGATTTGGCC
 FCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACA
 TTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCTTTCCCAGCT CTGATTACĞCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTTGCAGACGCGTTACGT **GGCGTAATAGACGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAAGCCTG** > E-130 m37 SZ

rggtggtgggcacctgtaatcccagttacttgggaggctgaggcaggagaaatttcttgaacctggaaggcagagg GTCAGGAGTTCTAGATCAGCCTGGCCAACAGGGTGAAACCATGTCTCTACTAAAAATACAAAATTAGTCAGGCG TTGCAGTCAGCCGAGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTTCT ICGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCACAGTTGCGCAGCCTGAATGGCGAATG CTATCČCAŤGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCG AGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACT GGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCTGGCGTTAÇCCAACTTAATCGCCTTGCAGCACATCCCCTT > E-140 m48 SZ

GTTACGTATCGGATCCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCCAAATCAGATGGATCATCTG CTATGACCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGC > E-150 m48 SZ

Figure 3

TAGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACT ATCATGGCAAATGCTTGTCATCCTAGCTACTCAGAAGGCTGAGGCAGAGGAATCACTTGAACCTGTGAGGCGGAG GITTCGGTGAGCTGAGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTTC GGCCGTCGTTTTACAACGTCGTGAAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCT AGĠTCAGGAGTTCAAGAACCACCTTATCAACATGAAGAATCCTGGTCTCTACTAAAAGTACAAAATTAGCCAGGT TTCGCCAGCTGGCGTAATAGCGAAGAGGGCCGCACCGATCGCCCTTCCAACAGTTGCGCAGCCTGAATGGCGA

ACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCG ATGATTACGCCAAGCTCTAATACAACTCACTATGGGCAAATGGTCGCAACCTCGCATGCTGCATACGCGTTACGTA CTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGAAATT TCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACTGCAACCTCCACCTCCCAGGCTCAATG TTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCTTTCGCCAG CTGITGAGATGGGGTITITGCCATGITTGCCCAGGCAGGTCTCGAACTGCTGGGCTCAAGTGATCCTCCTGCCTCCAC CTCACAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGGCTAGACCAC ATCCTCCCACCTCAACTCCCCCGAGTAACTGGGACCACAGGTGCCAGCATGCCCAGCATGCCCAGCTAATTTTGTATTTT GTAAGCGTTAATAT

CAGACGCGTTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTTGGCTCACTGCAACCTCCGC TGCCCGCCTCAGCCTCCCAAACTTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCT CTAGITITITGIAITITITAGIAGAGAIGGGGITITCCCCAIGIIGGCCAGGAIGAICTCGAICTCTIGACCTCGIGAIC TTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACAT AGCTCTAGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAA AAGATCCATATGACCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTG CTCCCGGGTTCAAGAGATTCTCCTGCCTCAGCCTCCGAGAGGCTGGGACTACAGGCATGCGCCACCATGCCCAG CCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAG

TCGGATCCAGAATTCGTCGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACGTGTGG GGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTTTACAA CGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCTTTCGCCAGCTGGCGTA ATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGAAATTGTAAGCGT ATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTA TAATATITITGITAAAATICGCGTTAAATITITGITAAATCAGCTCATTITITAACCAATAGGCCGAAATCGGCAAA Figure 3 Continued

CCTAATCAAGTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGC <u>AAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCAC</u> **TTGACGGGGAAAGC**

> E-221_m37_SZ

GCGTTACGTATCGGATCCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCCAAATCAGATGGATCATC AGGITTCGGTGAGCTGAGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGGCTAGGCTAGG TCTAGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCA **IGAGGTCAGGAGTTCAAGAACCACCTTATCAACATGAAGAATCCTGGTCTCTACTAAAAATACAAAATTAGCCAG** 3TATCATGGCAAATGCTTGTCATCCTAGCTACTCAGAAGGCTGAGGCAGAGGAATCACTTGAACCTGTGAGGCGG CTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCC CCATATGAČCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGAC

> E-244 m48 SZ

GCGTTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCAC AGGITCAAGIGAITCCICIGCCICAGCCITCIGAGIAGCIAGGAIGACAAGCAITTGCCAIGAIACCIGGCIAAIT ITGTATTTTAGTAGAGCCAGGATTCTTCATGTTGATAAGGTGGTTCTTGAACTCCTGACCTCAGATGATCCATCT CCGTATGACCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGAC GGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACACCT AGACCACACGTGTGGGGCCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACT TTCGCCAGCTGGCGTAATAGCGAAGAGGCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATG

> E-246 m48 SZ

ITGTATTTTTACTAAAGACGGGTTTTGCCATGTTGGCCAGGCTGTTCTCAAACTCCTGACTTCAGGTGATCCACCT CGTTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCGGCTCACTGCAACCTCCACCTCCAC 3GCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCT CTATGACCATGATTACGCCAAGCTCTAATACCGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACG GGTTCAAGCAATTCTCCTGCCTCAGCCTCCCAAGTAGCTGAGATTACAGGCGGCTGCCATCATGCCTGGCTAATTT AGACCACACGCGGGGGCCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACT TCGCCAGCTGCCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGT

> E-251_m48_SZ

AGTAGAGGCGGGGTTTCACCATGTTGGCCAGGCTGGTCATGAACTCCTGACCTCAGGTGATTCACCTGCCTCAGGC ATCGGATCCAGAATTCGTGATTCGGAGGGTGTTTGCACAATCTTGACTAACTGCAACATCTGCCTCCCAGGTTCAA GCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTTTACAACG TCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAAT TCCCAAACTGCTGGGAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACGTGTGGGG GCAATTCTGCCTCAGCTTCCTGAGCAGCTGGGATTACAGATGAGCACTACCATGACAGGCTAATTTTTATATTTTT CATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGI **AGCGAAGAGGCCCGCACCGATCGCCCTTCC**

> E-252 m48 SZ

GCGTTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCAC TIGIATITITIAGTAGAGCCAGGATICTICATGTIGATAAGGIGGTICITGAACTCCTGACCTCAGATGATCCATCT GGCCGTCGTTTTACAACGTCGTGACTGGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCC GATTTGGCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGGCTAGGCTAGGCTAGCTCT CGATATGAČCATGATTACGCCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGAC AGGTTCAAGTGATTCCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATT AGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACT TTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCTTCCC

> E-2531 m48 SZ

CCTGAGGTCAGGAGTTCATGACCAGCCTGGCCAACATGGTGAAAACCCCGCCTCTACTAAAAATTAAGC ATGTTGCAGTTAGTCAAGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGGCCTAGGCTAGG TCTAGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCA CTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCC CAGCTĀTGĀCCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGA CTGTCATGGTAGTGCTCATCTGTAATCCCAGCTGCTCAGGAAGCTGAGGCAGAATTGCTTGAACCTGGGAGGCAG CGCGTTACGTATCGGATCCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCTGAGGCAGGTGAATCA CTTTCGCCAGCTGGCGTAATAGCGAAGAGGGCCGCACCGATCG

> E-2532 m48 SZ

GTTACGTATCGGATCCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCTGAGGCAGGTGAATCACCTG TTGCAGTTAGTCAAGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCT CTATGACCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGC AGGTCAGGAGTTCATGACCAGCCTGGCCAACATGGTGAAACCCCGCCTCTACTAAAAATATAAAATTAGCCTGT CATGGTAGTGCTCATCTGTAATCCCAGCTGCTCAGGAAGCTGAGGCAGAATTGCTTGAACCTTGGGAGGCAGATG AGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACT

GGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCT TTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTNCCAACAGTTGCGCAGCCTGAATGG

> E-258 m48 SZ

CAGGITICAAACGATICICCIGCCICAGCCICCCGAGIAGCIGGGAITAIAGGCACCIGCCACCACGCCCAGGIAAI ITITIGCATITITIAGIAGAGGGGTTICACIATGTIGGCCAGGCTGGTCTAGAACTCCTGACCTTGTGATCCGCC CGCCTTGGCCTCCCAAACTGCTGGGAGTAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACC ACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGT CGCGTTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTTGGCTCACTGCAACCTCTGCCCCC <u> CCATATGATCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACCGCATGCTGCAGA</u> CGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAAC

> E-261 m50 Ctrl

CCACACGTGTGGGGGCCCGAGCTCGGGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCC ATITITAGIAGAGCAGGAITCITCAIGITGAIAAGGIGGITCITGAACICCIGACCICAGAIGAIGAICCAICIGAII ACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTCGCACAATCTCAGCTCACCGAAACCTCCGCCTCACAGGT TCAAGTGATTCCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTTGT TGGCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGGCTCTAGA TGACCTTGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTT GTCGTTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCC

> E-267 m50 Ctrl

CTGAGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACG TCAAGAACCACCTTATCAACATGAAGAATCCTGGTCTCTACTAAAAATACAAAATTAGCCAGGTATCATGGCAAA TGCTTGTCATCCTAGCTACTCAGAAGGCTGAGGCAGAGGAATCACTTGAACCTGTGAGGCGGAGGTTTCGGTGAG TGIGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTT <u>TTACGČCAĀGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGG</u> ATCCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCCAAATCAGATGGATCATCTGAGGTCAGGAGT TACAACGTCGTGACTGGGAAAACCCTGGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCTTT

> E-269 m50 Ctrl

ATTGGATCCAGAATTCGCGATTGGAGGGTGTTTGTACAATCTCTGCTCACCGAAACCTCCGCCTCACAGGTTCAAG TGATCCCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTTGTATTTTT CTTCCĂAAĞGNTAAGNTCTAATATTACTCACTATAGGGAAAGCTCGGCCCCACTCATGCTGCAGACGCGTTACGT CCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCAACAAGCTTCT

GTCAGGAGTTCCAGACCAGGTTGACCAACATGGAGAAACCCTGTCTCTACTAAAAATACAAAATTAGCCAGGTGT ATTGGTGCGTGCCTGTATTCCCAGCTACTTGGGAGGCCGAGGCAGGAGAATCGCTGGAACCCAGGAGGCGGAGGT GACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTG <u>GGTGAGAGTTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTT</u> ACGTATCGGATCCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCTGAAGTGGGTTGATTACCCGAG GCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCTT TCGCCAGCTGGCGTAATAAGCGAAGAGGCCCGCACCGATCGCCCTTTCCAACAGTTGCGCAAGCCTGAATGGCG > E-285 m56 SZ

ATTCTTCATGTTGATAAGGTGGTTCTTGAACTCCTGACCTCAGATGATCCATCTGATTTGGCCTCCCAAACTGCTGG GACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCG CAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTTGTATTTTAGTAGAGACCAGG GAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACGTGTGGGGGCCCCG AGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCCGCACAATTCACTGGCCGTCGTTTTACAACGTCGT GTTCTĀATĀCGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGGATCCAGAAT TCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCACAGGTTCAAGTGATTCCTCTGCCT <u> AAGAAGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGAAATTGTAAGCGT</u> > E-286 m56 SZ

> E-287 m56 SZ

TATCAACATGAATAATCCTGGTCTCTACTAAAATACGAAATTAGCCAGGTATCATGGAAAATGCTTGTCATCCTA TAATTÄACTCACTATAGGGAAAGCTCGGGAGCACGCATGCTGCAUACGCGTTTCGTATCTGGATCCAGAATTCGC GATTGCCTGTACTCCCAGCAGTTTGGGAGGCCAAATCAGATGGATCATCTGAGGCCAGGAGTTCAAGAACCACCT AACACCCTCCAATCTGAATTCGTCCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACGCGTGGGGGGCCC GCTACTCAGAAGGCTGAGGCAGAGGAATCACTTGAACCTGTGAGGCGGAGGTTTCGGTGAGCTGAGATTGGGCA GAGCTCGCGGCCGCTGTATTCTATT

> E-288 m56 SZ

GAGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACGTG AAGAACCACCTTATCAACATGAAGAATCCTGGTCTCTACTAAAAATACAAAATTAGCCAGGTATCATGGCAAATG CTTGTCATCCTAGCTACTCAGAAGGCTGAGGCAGAGGAATCACTTGAACCTGTGAGGCGGAGGTTTCGGTGAGCT GTTCAĞATČTAATANGACTCACTATCGGGAAAGCTCGGCACCACGCATGCTGCAGACGCGTTACGTATCCGGATC CATGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCCAAATCAGATGGATCATCTGAGGTCAGGAGTTC

IGGGGGCCCGAGCTCGCGGCCGCTGCATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTTT

> E-289 m56 SZ

CTGAGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACG IGTGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGGCCGTCGTT TGCTTGTCATCCTAGCTACTCAGAAGGCTGAGGCAGAGGAATCACTTGAACCTGTGAGGCGGAGGTTTCGGTGAG | ICAAGAACCACCTTATCAACATGAAGAATCCTGGTCTCTACTAAAATACAAAATTAGCCAGGTATCATGGCAAA TTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCTTTCGCCAGCT TTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGG ATCCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCCAAATCAGATGGATCATCTGAGGTCAGGAGT 3GCGTAATAGCGAAGAGGCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGAAATTG

> E-290 m56 SZ

AGGTTGTGGTGAGCTGAGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGC CGAGGTCAGGAGTTACAGACCAGGTTGACCAACATGGAGAAACCCTGTCTCTACTAAAAATACAAAATTAGCCAG ICTAGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCA **FIGIATTGGTGCGTGCCTGTAATCCCAGCTACTTGGGAGGCCGAGGCAGGAGAATCGCTGGAACCCAGGAGGCG** GCGTTACGTATCGGATCCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCTGAAGTGGGTTGATTACC CTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCC ATATTGATČATGATTACGCCCAACGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGAC CTITCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCC

> E-291 m56 SZ

CACACCGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCC ACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCACAGGTT ITİTTAGTAGAGACCAGGATTCITCATGTTGATAAGGTGGTCCTTGAACTCCTGACCTCAGATGATCCATCTGATTT CAAGTGATTCCTCTGCCTCAGCCTTCAGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTTGTA GGCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCCTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGAC GTCGTTTTACAACNTCGTGACTGGGAAAACCCTGNCGTTACCCCACTTAATCNCCCTTGCAGCACATCCCCCTTTC GCCCAGNCTGGGCGTAATNANCGAANAGGCCCGCACCCGATCGCCCCT

> E-292 m56 SZ

CCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGGCAAATCAGATGGATCATCTGAGGTCAGGAGTTC ACGTCĀCGČTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGGAT

ACAACGTTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTTGCAGCACATCCCCCCTTTCGCCCAG 3AGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACGTT AAGAACCACCTTATCAACATGAAGAATCCTGGTCTCTACTAAAAATACAAAATTAGCCAGGTATCATGGCAAATG GTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGGCGCACAATTCACTGGCCGTCGTTTT CTTGTCATCCTAGCTACTCAGAAGGCTGAGGCAGAGGAATCACTTGAACCTGTGAGGCGGAGGTTTCGGTGAGCT

> E-293 m56 SZ

GTTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCACAG ATTTGGCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGGCTAGGCTAGCTCTA GGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCT TATGAČCAŤGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTTGCAGACGC GACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTG GTATTITTAGTAGAGCCAGGATTCTTCATGTTGATAAGGTGGTTCTTGAACTCCTGACCTCAGATGATCCATCTG GTTCAAGTGATTCCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTI TTCGCCAGCTGGCGTAATAGCGAAGAGGCCGCACCCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATG

> E-294 m740 SZ

ATCCAGAATTCGTCGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCACAGGTTCAAGTGAT TCCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTTGTATTTTAGTA TGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTTTA CAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGC AAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACGTG TTACGCCACGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGG GAGACCAGGATTCTTCATGTTGATAAGGTGGTTCTTGAACTCCTGACCTCAGATGATCCATCTGATTTGGCCTCCC 3TAATAGCGAAGAGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAG

> E-295_m740_SZ

GTTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCACAG ATTTGGCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGGCTAGCTCTA 3GGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCC IATGAČCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTTGCAGACGC GTATITITAGIAGAGCCAGGATICITCATGITGATAAGGIGGITCITGAACICCTGACCICAGAIGAICCATCIG GACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGGCCGCACAATTCACT **GTTCAAGTGATTCCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTT** TTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTTGCGCAGCCTGAA

> E-296 m57 Ctrl

CATGTTGCCCAGGCTGGTCTCGAACTCCTAACCTTGTGATCTGCCCACCTCGGCCTCCCAAACTGCTGGGAGTACA CAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGGATCCAG GGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACGTGTGGGGGGCCCGAGCTCGC GGCCGCTGTATTCTATAGTGTCACCTAAATGGGCCGCACAATTCACTGGGCCCGTCGTTTTACAACGTCGTGACTG GGAAAACCCTGGGCGTTACCCAACTTAATCGCCCTTGCAGCACATCCCCCTTTCGCCAGCTTGGC

> E-297 m740 SZ

TTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCACAGG **CCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCC** ITCAAGTGATTCCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTTGT ATITITAGTAGAGCCAGGATTCTTCATGTTGATAAGGTGGTTCTTGAACTCCTGACCTCAGATGATCCATCTGATT **CCAGCTGGCGTAATAGCGAAGAGGCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGAA** GTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCG
 TATGACCATCATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCG
 1GGCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGA

> E-298 m57 Ctrl

AGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCACAGGTTCAAGTGATTCCTC TGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTTTGTATTTTTAGTAGAGA GGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCCTAAATGGCCGCACAATTCACTGGGCCGTCGTTTTAC GTCCCGATCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGGATCC CCAGGATTCTTCATCGTTGATAAGGTGGTTCTTGAACTCCTGACCTCAGATGATCCATCTGATTTGGCCTCCCAAA CTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACGTGTGG **AACGTCGTGACTGGGAAAACCCTGGGGCGTTACCCCCAACTTAATCG**

▷ E-299 m57 Ctrl

GTCAAĞATCGAATAGGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCCGACGCGTTACGTATCGGATCC AGAATTCGTGATTGCCTGTACTCCCAGCACTTTGGGAGGGCAAATCAGATGGATCATCTGAGGTCAGGAGTTCAA GAACCATCCTTATCAACATGAAGAATCCTGGTCTCTACTAAAAATACAACATTAGCCAGGTATCATGGCAAATGC TTGTCATCCTAGCTACTCACAAGGCTGAGGCAGAGGAATCACTTGAACCTGTGAGGCGCAGGTTTCGGTGAGCTG

AGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTCTCTCGAGCCTAGGCTAGCTTTAGANCACACGTG TGGGGGC

5> E-300 m57 Ctrl

CAATTCTGCCTCAGTTTTCTGAGCAGCTGGGATTACAGATGAGCACTACCATGACAGGCTAATTTTTATATTTTAC ATCGGATCCAGAATTCGTGATTGGAGGGCGTTTGCGCAATCTTGACTAACTGCAACATCTGCCTCCCAGGCTCAAG TAGAGGCGGGGATTCACCATGTCGGCCAGGTTGGTCATGAACTCCTGACCTCAGGCGATTCACCTGCCTCCGCCTC GTTGAĀACGĀCAAGATCTAATACGACTCACTATAGGGAAAGCTCGGCACTACGCATGCTGCAGACGTGTTGACGT CCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAG

E-304 m57 Ctrl

CTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTTGTATTTTAGTAGA rccagaattcgtgattggagggtgtttgcacaatctcagctcaccaaacctccgcctcacaggttcaagtgattc GGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCCGCACAATTCACTGGCCGTCGTTTTAC CTACGTACGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGGA GACCAGGATTCTTCATGTTGATAAGGCGGTTCTTGAACTCCTGACCTCAGATGATCCATCTGATTTGGCCTCCCAA ACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGGCTAGGCTAGCTCTAGACCACACGTGTG **AACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGC**

> E-305 m740 SZ

CCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTTGTATTTTAGTAG ATCCAGAATTCGCGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCACAGGTTCAAGTGATT TGGGGGCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTTTTA **AACTGCTGGGAGTÄCAGGCAATCTGAATTCGTCGACAAGCTTCTCCGAGCCTAGGCTAGCTCTAGACCACACGTG** TTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGG AGACCAGGATTCTTCATGTTGATAAGGTGGTTCTTGAACTCCTGACCTCAGATGATCCATCTGATTTTGGCCTCCCA

E-308 m74 SZ

CCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATTTTGTATTTTAGTAG ATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAATCTCCGCCTCACAGGTTCAAGTGATT TTACGTCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGG AGACCAGGATTCTTCATGTTGATAAGGTGGTTCTTGAACTCCTGACCTCAGATGATCCATCTGATTTGGCCTCCCA 4ACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACGTGT GGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTT

TGAGATTGCGCAAACACCCTCCAATCTGAATTCCTCTGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCCACG GCTTGTCATCCTAGCTACTCAGAAGGCTGAGGCAGAGGAATCACTTGAACCTGTGAGGCGGAGGTTTCGGTGAGC _AGGCA<u>Ā</u>GA<u>T</u>CTAATACGACTCACTATAGGGAAACGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGGAT CAAGAACCACCTTATCAACATGAAGAATCCTGGTCTCTACTAAAAATACAACATTAGCCAGGTATCATGGCAAAT CCAGAATTCGTGATTGCCTGTACTCCCACGCAGTTTGGGAGGCCAAATCAGATGGATCATCTGAGGTCAGGAGTT TGTGGGGGCCCGAGCTCGCCGTCGTATTTCTATAGTCGTC > E-309 m74 SZ

E-310 m74.SZ

GATCCAGAATTCGTGATTGGAGGTGTTTGCACAATCTCAGCTCACTGCAACCTCTGCCTCTCAGGTTCAAGTGAT TCTCCTGCCTCATCCTCCCCAGTAGCTGGGTTTACAGGCATGCACCACCACAGCTGGCTAATTTTTGTATTTTAGT AGAGATGGGGTTTCACCATGTTGGACAGGCTAGTCTTGAACTCCTGACCTCAAGTGATCCACCCGCCTCAGGCCTCT TTACGTCACCGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCG CAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACGGT TTACAACGTCCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAA

> E-311 m74 SZ

CGAGACCAGCCTAGCCAACATGGTGAAACCCTGTCTCTACTAAAATACAAAATTAGCCAGGCAAGGCAGCAC ACTGAGATTGTGCAAACACCCTCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGGCTCAGACCACGG TGTGGGGGCCCGAGCTCGCCGGCCGCTGTATTCTATTAGTGTCACCTAAATGGGCCGCACAATTCACTGGCCGTCC <u>AAACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGG</u> ACGCCTGTAATTCCACCTACTCGGGATGCTGAGGCATGAGAATCGCTTGAACCTGGGAGGTGGAGCTTGCAGTGA GTTTTACAACGTCGTGACTGGGAAAACC

> E-312 m74 SZ

CAAACACCCTCCAATTTGAAATTCGTCGACAAGCTTCTCCGAGCTCTAGGCTAGCTCTAGACCCACACGTGTGGGG TATCAACATGAAGAATCCTGGTCTCTACTAAAATACAAATTAGCCAGGTATCATCGGCAAATGCTTCGTCATCC
 IAGCTACTCAGAAGGCTGAGGCAGAGGAGTCACTTGAACCTGTGAGGCGGAGGAAACGGCGAGATGAGATTGTG
 GATTGCCTGTACTCCCAGCAGTTTGGGAGGGCAAATCAGATGGATCATCTGAGGTCAGGAGTTCAAGAACCACCT CGAATĀCGĀCTACTATACGGAAAGCTCGGTACCACGCATGCTGCACGCGTTACGCATCGGATCCAGAATTCGT GCCCCGAGCTCGCG

> E-313_m74_SZ

AAAAAAAAAATTAGCCTGGCATGGTGGTGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCACGAGAATC CTTCTCGAGCCTAGGCTAGCTCTAGACCACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCAC CTAAATGGCCGCACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAA GCTTGAACCCGGTGGGCAAGGGTTGCAGCGATCCGAGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAG TATGACATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGT TACGTATCGGATCCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCTGAGACAGGTGGAACACTTGA TCGCCTTGCAGCACATCCCCC

> E-315 m74 SZ

TGaTTĀCGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATC ACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGG GGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCGGCTCACTGCAACTTCTGCCTCCTGGGTTCACACTG GTAGAGAAGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGATCTCCTGATATTGTGATCCACCCGCCTCGGCCTCT CAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACGT GTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTT CGTAATAGCGAAGAGGCCGCACCGATCGCCCTTCCCAACAGTTGCGC

> E-314 m74 SZ

ACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGG GTAGAGAAGGGGTTTCACCGTGTTAGCCAGGATGGTCTCGATCTCCTGATATTGTGATCCACCCGCCTCGGCCTCT <u>ATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGAÇGCGTTACGTATCG</u> GATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCGGCTCACTGCAACTTCTGCCTCCTGGGTTCACACTGT CAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACGT GTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTTT TCTCCTGCCTAAGCCTCCCAAGTAGCTGGGACTACAGGCGCGTGCCACCATGCCCGGCTAATTTTTGTATTTTTA CGTAATAGCGAAGAGCCGCACCGATCGCCCTT

4> E-319 m74 SZ

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AATTCACTGGGCCGTCGTTTTACAACGTCGTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCA CATCCCCTTTCGCCAGCTGGCGTAATAACGAAGAGGCCGCACCGA

TITIGITAAAATICGCGITAAATTITIGITAAATCAGCICATITITTAACCAATAGGCCGAAATCGGCAAAATCCCT TATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAAC TGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGC GTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCA GAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGAAATTGTAAGCGTTAATA AFGATTÁCGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTA TCGGATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACGTGTGGGGGGCCCGAGCTCGC GGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTTTACAACGTCG AGTITITIGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCC

CTCGGCCTCTCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGGCTAGGCTAGCTCTAG TATGAČCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCG TTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCGGCTCACTGCAACTTCTGCCTCCTGGG ACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGG GCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTT TGTATTTTTAGTAGAGAGGGTTTCACCGTGTTAGCCAGGATGGTCTCGATCTCCTGATATTGTGATCCACCGG TTCACACTGTTCTCCTGCCTAAGCCTCCCAAGTAGCTGGGACTACAGGCGCGTGCCACCATGCCCGGCTAATITIT TCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATG

GGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTTTACA ACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCTTGCAGCACATCCCCCCTTTCGCCAGCTGGCGT GATGGGGTTTCACTATGTTGCCCAGGGTGGTCTCAAACTCCTGACCTCAAGTGATCCACCTGCTTCAGCTTCCCAA ACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACGTGTG ACGTAČGCTČTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGGATC CAGAATTCGTGATTGGAGGGTGTTTGCACAATCTTGGCTCACTGTAACCTCTGCCTCCTGGGTTCAAGTAATTCTC ATAGCGAAGAGCCCGCACCCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGAAATT

7]> E-323_m74_S

ATCGCACCCATAGTCCCTGCTAATCAGGAGGCTGAGCTTGAACATGGGAGGTGGAGGCTGCAGTGAGCTGAGAT IGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACGTGTGGGG <u>AAACGCAAGCTCTAATACGACTCACTATAGGGAAAGTTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGGA</u> ICCAGAATTCGTGATTGCCTGTACTCCCAGCACGTTTGGGAAGCCGAGGTGGGAAGATCGCTTCGAGGTCAGGAG ITCAAGACCAGCCTGGCCAACATGGCAAAACCTCGTCTATACAAAATACAAAACTTAGCCAGGCCGTGTTGGC GCCCGAGCTCGCGGCCGCTGTATTCTATAGT

4> E-324 m74 SZ

GGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGGCCGCACAATTCACTGGCCGTCGTTTTAC <u>AACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCTTTCGCCAGCTGGCG</u> AGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACTGCAACCTCCACCTCTACGACTCAAGTGATTATCC GACGGAȚTTTCACCATGTAGCCCAGGCTGGTCTCAAACTCCTGAGCTTAAGCGATCCACCTTCCTGGACCTCCCAA ACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACGTGTG GTTAAGATCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGGATCC <u> FAATAGCGAAGAGGCCGCACCGATCGCCCTTCCCACAGTTGCGCAGCCTGAATGGCGAATGGAAATTTAA</u>

1 > E-325 m74 SZ

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3]> E-149 m48 SZ

ATTITTAGCAGAAATGGGGTTTCCCCATGTTGACCTGGCTGGTCTCGAACTCCTGACCTTGTGATCTGCCCGCCTTG <u> ACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGT</u> <u> ACGCTTÖCAÄGGATTCAACAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGC</u> TGCAGTGATTCTCCTGTCTCAGCCTCCCAAGTAGCTGGCATTACAGGTTCCCACCACTACACCCAACTAATTTTGT CGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCC GCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACC GTTACGTATCGGATCCAGAATTCGTGATTAGGGTGTTTGCACAATCTCGGCTCATTGTAACCTCTGCCTCCAGGT \GCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGA

ATTCCTCTGCCTCAGCCTTCTGAGTAGCTAGGACGACAAGCATTTGCCATGATACCTGGCTAATTTTGTATTTTAG CCAAA CTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACACG <u> SATTACGCCAAGCTCTAATACTACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATC</u> GGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCACAGGTTCAAGTG **FACAACGTCGTGACTGGGAAAACCTG** 3> E-302 m57 Ctrl

3> E-119m57Ctrl

<u> AGGTATGGTGGTACTTGCCCGTAATCCCAGCTATTCAGAAGGCTGAGGCAGGAGAGTCACTTGAACCCAGGAGTC</u> <u> LAGCTATGACCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGA</u> CCTGAGGTCGGGAGTTCGAGAACCGCCTGACCAACATGGAGAAAACCCCGTCTCTGCTAAAAATACAAAATTAGCT ITCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACA CGCGTTACGTATCGGATCCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCAGAGGCAGGTGGATCA AGCTCTAGACCACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAA CCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAAT AGAGGTTGCAGTCAGCTGAGATTGTGCAAACACCCTCCAATCTGAATTCGTCGACAAGCTTCTCGAGGCTAGGCT **3GCGAATGG**

[]> E-120m57Ctrl

CCTGCCTCAGACTCCGAAACTGCTGGTAGTACAGGCAATCTGCATTCGTCTGCATTCTTCTACAGCCTAGGCTAGG TATAGACCACACTTGACCACGGCCCGAGCTCCCGGCCGCTTGGATTCTATAGTGTCATATAAAGGCCCGAACAATT CCTCCGGGTTCCAGGTGTTGCTAGTGTTTGAACCTCCTGAGCATCATTGGATAACAGTAGCCTCTCACCATGCTCA <u>|CTTGTGCTTGTATTGGTGGCAGCGGTCCACCATGCCGGTTATGCTGAACTCGGACTCATCACCTTAAATTAACCA</u> <u> AATAGCTATGCCCATGATTACGCCCAAGCTCTAATACGACTCACTATAGGGTATGCTCGGAGCTAGGCATGCTGCA</u> CACTGCACCGTAGTTT

Sorry, no matches found

5> E-166m50Ctrl

GACGCGTTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCGGCCCACTGCAACCTCCGCCT CCCGGGTGCAAGCAGTTCTCCTACCTCAGCCTCCTGAGTAGCTAGGATTACAGGCACACCTGGCTAATTTTGTGGT AACAGCTATGACCATGATTACGCCAAGCTCTAATACGACŤCACTATAGGGAAAGCTCGGTACCACGCATGCTGCA TTTAGTAGAGACGGCGTTTCACCATGTTGGCTAGGCTGGTCTCGAACTCCTCACCTCAAATGATCCACCTGCCTCA

AGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGAAAT ACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGI CGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCC 3CCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACC **IGTAAGCCGTTAATA**

2> E-167m50Ctrl

3CGTTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCGAAACCTCCGCCTCAC TIGTATITITAGTAGAGCCAGGATTCTTCATGTTGATAAGGTGGTTCTTGAACTCCTGACCTCAGATGATCATCT GATTTGGCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGGCTAGCTCT 3GCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCT ACTITATGACATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGAC AGGTTCAAGTGATTCCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAGCATTTGCCATGATACCTGGCTAATT **AGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAĠTGTCACCTAAATGGCCGCACAATTCACT** ITCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCTTCCCAACAGTTGCGCAGCCTGAATG

5> E-169m50Ctrl

CGAGGTCAGGAGTTCCAGACCAGGTTGACCAACATGGAGAAACCCTGTCTCTACTAAAAATACATAATTAGCCAG GCGTTACGTATCGGATCCAGAATTCGTGATTGCCTGTACTCCCAGCAGTTTGGGAGGCTGAAGTGGGTTGATTACC 3TGTATTGGAGCGTGCCTGTATTCCCAGCTACTTGGGAGGCCGAGGCAGGAGAATCTGCTGGAACCCACGATGGC GGAGGTTGTGGAGAGCTGAGATTGTGCAAACACCCTCCAATCTGAATTCGTCTACAAGCTTCTCGAGCCTAGGTTA AAGCTTGACCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGAC GCTCTAGACCACACGTGTGGGGGCCCGAGCTCGCGGACGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAAT CACTGGCCGACGTTTTACAACGTGGTG

2> E-270m50Ctrl

TGAAGAATCCTGGTCTCTACTAAAAATACAAATTAGCCAGGTATCATGGCAAATGCTTGTCATCCTAGCTACTCA GAAGGCTGAGGCAGAGGAATCACTTGAACCTGTGAGGCGGAGGTTTCGGTGAGCTGAGATTGTGCAAACACCCTC **ACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCG CACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGAAATTGTAAGCGTTAATATTTTGTTAAAAT** CCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAA GTACTCCCAGCAGTITGGGAGGCCAAATCAGATGGATCATCTGAGGTCAGGAGTTCAAGAACCACCTTATCAACA CAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGCTCTAGACCACGTGTGGGGGCCCGAGCTCGCGG CTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGGATCCAGAATTCGTGATTGCCI

CCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCACTGGCC TIGCCCATGCTTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCÁTGCTGCAGACGCGTT CAAGCGATTCTCTGGACTCAGCCTCCTGAGTAGCTGGAATTACAGGGATTCGCCACCATGCCCAGCTAATTTTGTA ACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACCATGACCTCTGCCTCTGGGTT GTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCTTTCG TGGCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGGCCTAGGCTAGCTCTAGA CCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGA 6> E-271m50Ctrl

0> E-272m50Ctrl

AATTTTTGTATTTTTAGTAGAGACAGAGTTTCACCATGCTGGCCAGGCTGGTCTCAAACTCCTGCCCTCAGATGTTC CACCCACCTTGGCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTA GCTCTAGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATT AGACGCGTTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCTCAGCTCACTGCAGCCTCCTCC CACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACÇCAACTTAATCGCCTTGCAGCACATCC CAATACCGCTTGACCATGATTACGCCAAGCTCTAATACGACTACTATAGGGAAAGCTCGGTACCACGCATGCTGC CCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCAACAGTTGCGCAGCCTG

2> E-273m50Ctrl

CAGCTCACCGAAACCTCCGCCTCACAGGTTCAAGTGATTCCTCTGCCTCAGCCTTCTGAGTAGCTAGGATGACAAG AGCTICTCGAGCCTAGGCTCTAGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTC CATTIGCCATGATACCIGGCIAATITIGIAITITIAGIAGAGCCAGGATICITITATGITGATAAGGIGGITCTIGA ACTCCTGACCTCAGATGATCCATCTGATTTGGCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACA GCTCGGTACCACGCATGCTGCAGACGCGTTACGTATCGGATCCAGAATTCGTGATTGGAGGGTGTTTGCACAATCI ACCTAAATGGCCGCACAATTCACTGGCCGGCGTTTTACAACGTCGCGACTGGGAAAACCCTGGCGTTACCCAACT **FAATCGCCTTGCAGCACATCCCC**

2> E-275m50Ctrl

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0> E-279m50Ctrl

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2> E-281m50Ctrl

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2> E-283m56SZ

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2> E-284m56SZ

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7> E-61m34BD.

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2> E-62m34BD

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2> E-63m34BD

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| CTAGACCACACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATTCA CTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCC ICTGACTTGGCCTCCCAAACTGCTGGGAGTACAGGCAATCTGAATTCGTCGACAAGCTTCTCGAGCCTAGGCTAGG CTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCTTCCCAACAGTTGCGCAGCCTGAATGGCGA

2> E-66m39MD

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2> E-68m39MD

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3> E-71m39MD

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3> E-74m43BD

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> E-75m43BD

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> E-78m43BD

A C G C G TTA C G TA T C C A G A A T T C G T G A T T G G A G G T T T G C A A T C T C G G C T C A A T C C A A C ITITIGIAITITTAGIAGAGACAGGGITTITGCCAIGITGGCCAGGCIGGICTCAAACICCTGACCTCAGGIGGICCA *GCTCTAGACCACGTGTGGGGGCCCGAGCTCGCGGCCGCTGTATTCTATAGTGTCACCTAAATGGCCGCACAATT* CTGGGTTCAAGCAATTCTCCTGTCTCAGCCTCCGAGTAGCTGGGATTACAGGCACATGCCACCATGCCCAACTAA CACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCC **ACAGCTATGACCATGATTACGCCAAGCTCTAATACGACTCACTATAGGGAAAGCTCGGTACCACGCATGCTGCAG** CGGCCTCAGCCTCCCAAACTGCTGGGAGTACAGGCCAATCTGAATTCGTCGACAAGCTTCTCGAGGCTAGGCTA CCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCTTCCAACAGTTGCGCAGCCTGAA

> E-79m43BD

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> E-83m43BD

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> E-167m50Ctrl

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> E-271m50Ctrl

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> E-272m50Ctrl

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> E-273m50Ctrl

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> E-275m50Ctrl

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> E-279m50Ctrl

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> E-281m50Ctrl

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> E-283m56SZ

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> E-284m56SZ

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> E-61m34BD

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2> E-63m34BD

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2> E-66m39MD

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2> E-68m39MD

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3> E-71m39MD

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4> E-72m43BD

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3> E-74m43BD

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2> E-75m43BD

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3> E-78m43BD

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5> E-79m43BD

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3> E-83m43BD

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5> RevE-119m57Ctrl

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2> PK1601mM-13 m37-7+++

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2> PK1601mM-11 m37-5+++

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3> PK1601mM-60+++

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2> PK1601MM-59+++

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2> PK1601mM-58+++

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3[]> PK1601mM-57+++

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2> Pk1601mM-54+++

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2> pk1601mM-53+++

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5> nk1601mM-52+++

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]10> pk1601mM-37+++

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9> pk1601mM-35+++

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5> pk1601_mM-32+++

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4> pk1601_mM-31+++

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6> pk1601 mM-30+++

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7> pk1401 mM-24+++

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4> pk1401 mM-23+++

<u> CGÓTTICA TIGCA A CCICC GCITICCIA GGGICCA GIGA ICCTICCIGCCICA GICCCCCA A GIGGCIGGGA CIA CAGG</u> CATGTGCCACCACATCTGGCTAACTTTTGTATATTTAGAAACAGGGTTTCACCATGTTGGCCAGGCTGGTCTC GAACTCCTGGCCTCAAGTGATCCACCCGCCTTGGCCTCCC

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2> pk1401_mM-20+++

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2> pk1401_mM-19+++

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2> pk1401_mM-18+++

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2> pk1401_mM-17+++

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4> pk1401_mM-16+++

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2> pk1401 mM-14+++

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4> pk1401 mM-10-----

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2> pk1401 mM-8-----

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pk1401 mM-7-----

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pk1401 mM-6----

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pk1401 mM-5----

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PK1401 mM-4---

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pk1401_mM-3-----

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pk1401 mM-2----

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pk1401 mM-2-----

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BDc_m34-4----BD----

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SZb m37-10+++

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SZb m37-5+++

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SZb m37-3+++

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ВDс m34-10----ВD----

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SZb m37-2+++

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BDc m34-3----BD----

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BDc m34-1----BD-----

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pk211201 M39-2----BD----

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CtrlC m57-2----

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BDd_m43-19----BD----

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SZc_m37-26+++

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BDd_m34-19----BD-----

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BDd m34-14----BD-----

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BDd_m43-14---BD---

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SZc m37-15+++

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SZc m37-10+++

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SZc m37-7+++

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SZc_m37-5+++

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SZc m37-3+++

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pk0301 M39-14---BD---

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PK0301_M37-14+++

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PK0301 M37-11+++

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RevCompSZB_M37-6+++

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RevCompPK1401_mM-17+++

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RevCompPK1601mM-33+++

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RevCompPK1601mM-39+++

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CUTPK1601_mM-1_m57-6----

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CUTPK1601mM-55+++

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utPK1601mM-39+++

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CutPK1601mM-37+++

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CutPK1601mM-33+++

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CutPK1601_mM-31+++

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CutPK1401 mM-17+++

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CutPK1401 mM-2_1+++

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CutPK1401_mM-2_2+++

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CutSZB M37-6++

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CutSZB M37-3+++

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PK37-9RfWithM13R

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>PK37-9RrWithM13R

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GGCTGGTCTTGAATTCCTGGCCTCAAGAGATCCGCTGGCTTTGGCCTCTCAAACTGCTGGGAGTACAGGCAAGCCG AGCCTGAATGGCGAATGGACGCGCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGAC 3AATAGTAGCTGGGATTACGGGCGTGTGCCATCACACCCCAGCTAATTTTTGTATTTTTAGTAGAGACAGTTGTCCA GTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTT GCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGC GGAGGGTGTTTGCACAATCTTGGCTCACTGCAACCTCCACCTCGCAGTTCAAGCAATTCTTGTGCCTTAGCCTCCT 1>BD43-8(2)withM13R BD43-8 (178, 100, 11q22.3)

>BD43-9withM13R

CTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAA CTTAATCGCCTTGCAGCACATTCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCA TGAGTAGCTAGGACTATAGATGCCCCCACCACGCCTGGCTAATATTTTGTATTTTTTAGTACAGTCGGGGTTTTTGC GGAGGGTGTTTGCACAATCTCAGGTCACTGCAACCTTCGCCTCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCC ACAGTTGCGCAGCCTGAATGGCGAATGGACGCGCCCTGTAGCGGCGCATTAAGCCCGGCGGGTGTGGTGGTTAC

>BD43-10withM13R

GAGTAGCTGGAATTACAGACATGTACTACCACACCAGGCTAAGTTTTGTATTTTTAGTAGAGACGAGGTTTCACCA ATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCCGTGACTGGGAAAACCCTGGCGTTACCCAAC TTAATCGCCTTGCAGCACATCCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCC GGAGGGTGTTTGCACAATCTCAGGTCACTGCAACCTCCTCTTCTGCATTCAAATGATTCTCATGCCTCAGCCTTCC <u>AACAGTTTGCGCAGCCTGAATGGCGAATGGACGCGCCCTGTAGCGGCGCGTTAAAGCGCGGCGGCGGTGTGGTGGTTAA</u> IGTTGGCCAGGCTGGTCTTGAACTCCTGGCCTCAAGTGATCCACCTGCCTTGGCTTCCCAAACTGCTGGGAGTACA CGCGCAGCGTGACCGCTACACTTGCCAGCGCC

>BD43-14 (191, 100, 16q24.2) withM13R

GGAGGGTGTTTGCACAATCTCAGCTCACCACACCTTTTCCTGGTTGAGTGATTATCCTGCCTCAACCTCC

CAGTTGCGCAGCCTGAATGGCGAATGGACGCCCTGTAACGGCGCATTAAGCGCGGCGGGTGTGGTTACGC ATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCAACT TAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAA CGACTAGCTGGGATTACAGGCATGCACCACCATGCCTGGCTAATTTTGTATTTTAGCAGAGACAGTGTTTTCTCCA GCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGC

Figure 3 Continued

TGGCTCACTGCAACCTCCGCC-TCCCAGGTTCAAGC-AATTCTCCTGCCTCAG-TCTCCCGAGTAGCTGGGACTACCGGGGAGTGCTACCATGCCTGCGTAATTTTTGTACT IGGCTCACTGCAACCTCCGCC-TCCCAGGTTCAAGC-AATTCTCCTGCCTCAG-TCTCCCGAGTAGCTGGGACTACCGGGGAGTGCTACCATGCCTGCGTAATTTTTTGTACT lagetcaccacarcacc-tectgggttecagc-gaftctcetscetcgg-cetcccaagtagctgggattacaggcacgcaccaatacacctggctaattttg--tatt CAGCICACAACCICCGCC-ICCIGGGIICCAGC-GAIICICCIGCCICGG-CCICCCAAGIAGCIGGGAIIACAGGCACGCACCAAIACACCIGGCIAAIIIIG--IAII CAGCTCACCGCAACCTTIGCC-TCACGGGCTCAAGT-GATTCTCATGCTTGAT-CCTACCAAGTAGCTGGGATTACAGGGACATGCCATCATGAGCTAACTTTG-GTATT CACGTCACTGTAATGTCCATC-TCCCGGGTTCAGGT-GATTCTCCTGCCCCAG-CCTCCTGAGTAGCTG----TACAGGCGTGCACCACCATGCCCGACTAATTTT-GTACT CGGCTCAATGCAACCTCAGCC-ICCTGGGTICAAGC-AATTCICCTGTCTCAG-CCTCCCGAGTAGCTGGGGATTACAGGCACATGCCACCATGCCCAACTAATTTT-GTATT TGGCTCACTGTBACCTCTGCC-TCCTGGGTTCBAGT-BATTCTCCTGTCTCBG-CCTCCTGAGTAGCTAGGATTACTGGTGCCCGCCACCATGCCCGGCBAATTTT-GTATT IGGCICACTGIBACCICTGCC-ICCIGGGIICBAGI-BAIICICCIGICICAG-CCICCIGAGIBGGIIAGGAIIACIGGIGCCCGGCCACCAIGCCCGGCABAINITI-GIAII IGGCTCACTGCAACCTCTACC-TCCTGAGTTCAAGC-TCTTCTCCTGCCTCAA-CCTCCAGAGTAATTGTGATTACAGGTGCCTCCCACCACCACCAGGCTAATTTT-GTATT CAGCICACTGCAACCICCAIT-ICCIGGGIICAAGC-GAITCICCIGCCICAG-CCICCGGAGIAGCIGGGACCACAAGACGIGGCCACCAIGCCIGGGIAAIITIC-AIAII CAGCTCACTGCAACCACC-TCCCAGGTTCAAGT-GATTATCCTGCCTCAG-CCTCCCGAGTAGCTGGGATTACAGATGCCCAACACACACCAGGCTAATTTTTGTATT CAGCTCACTGCAACCACCACCATCCAGGTTCAAGT-GATTATCCTGCCTCAG-CCTCCCGAGTAGCTGGGATTACAĞATGCCCACCAACACACCAGGCTAATTTTTGTATT CAGCCCAGTGCAAGCTCCGCC-TCCCAGGTTCACGT-CATTCTCCTGCCTCAG-CCTCCCGAGTAGCTGGGGACTACAGGGGGCGCCCACCACGCCCAGCTAATTTTTGTATT CGGCTCACTGCAAGCTCCGCC-TCCCGGGTGCACGC-CATTCTCCTGCCTCAG-CCTCCCGAGTAGCTGGGAACTACAGGCGCCCGCCACCACGCCCGGCTAATTTTTGTATT TGGCTCACTGCAACCTCCGCC-TCCCAGGTTCAAGC-AATTCTCCTGCCTCAG-TCTCCCGAGTAGCTGGGAACTACCGGGGAGTGCTACCATGCCTGCGTAATTTTTGTACT CAGCICICCACAACCICCGCCAICGIGGGIICCAGCAGAIICICCTGCCICGG-CCICCCAAGIAGCIGGGAAIACAGGCACGCICCAAIAACACCIGGCIAAIIAIG--IAII cagctcaccgcaacctttgcc-tcacgggctcaagt-gattctcatgcttgat-cctaccaagtagctgggattacaggcacatgccatcatgctgagctaactttg-gtatt GGCCCACTGCAACCTCCGCC-TCCCGGGTGCAAGC-AGTTCTCCTACCTCAG-CCTCCTGAGTAGCTAGGATTACAGG------CACACCTGGCTAATTTTG--TGGT CAGCICACTGCAACCICCGCC-ICCIGGATICAAGC-GATITICCCGCCTIAG-CCICCIGAGTAACIGGGACIAGAGGAGGAGCAGCTACCACCCAGCTAATITIT-GIATI CGGCTCAATGCAACCTCAGCC-TCCTGGGTTCAAGC-AATTCTCCTGTCTCAG-CCTCCCGAGTAGCTGGGATTACAGGCACATGCCACCATGCCCAACTAATTTT-GTATI ch74-E52m/Sch74-E51m 1D43-E78m/BD43-E83m Ctrl50-RevE169m 3D43-RevE77m tr150-E166m

3ch74-E318m

BD43-E79m

tr157-E3m 3ch74-E318 Ctr157-E4m Ctr157-E6m ctr157-E6m

3D34-A14M

1D43-RevE7m

tr157-E5m 1D34-E62m 1D43-E78m 1D34-D19M

3D43-15m

3ch56-E283m

Sch56-r-37m

Sch56-E32m